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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=16; hr=16; min=49; sec=18; ms=192;]

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Application No: 10534772

Version No: 1.0

Input Set:

Output Set:

Started: 2008-07-16 14:41:20.943

Finished: 2008-07-16 14:41:23.801

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 858 ms

Total Warnings: 29

Total Errors: 0

No. of SeqIDs Defined: 29

Actual SeqID Count: 29

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-07-16 14:41:20.943
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Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 858 ms
Total Warnings: 29
Total Errors: 0
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> TOMLINSON, Stephen
HOLERS, V. Michael

<120> Complement Receptor 2 Targeted
Complement Modulators

<130> 577712000200

<140> 10534772

<141> 2008-07-16

<150> PCT/US2003/036459

<151> 2003-11-13

<150> US 60/426,676

<151> 2002-11-15

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1041

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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gagaaggact cagtgatctg ccttaagggc agtcaatggc cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cgggtactgt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 660
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gccaccacc tgaatgcaga ggaaaatctc taacttcaa ggtcccacca 780
acagttcaga aacctaccac agtaaatgtt ccaactacag aagtctcacc aacttctcag 840
aaaaccacca caaaaaccac cacaccaa atgtcaagcaa cacggagtac acctgtttcc 900
aggacaacca agcatttttc tgaacaacc ccaaataaag gaagtggaac cacttcaggt 960
actaccgtc ttctatctgg gcacacgtgt ttcacgttga caggtttgct tgggacgcta 1020
gtaaccatgg gcttgctgac t 1041
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<210> 2

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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Glu	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Val	Leu	Leu	Cys	Leu	Pro	Ala	Val
			20					25					30		
Trp	Asp	Cys	Gly	Leu	Pro	Pro	Asp	Val	Pro	Asn	Ala	Gln	Pro	Ala	Leu
		35					40					45			
Glu	Gly	Arg	Thr	Ser	Phe	Pro	Glu	Asp	Thr	Val	Ile	Thr	Tyr	Lys	Cys
	50					55					60				
Glu	Glu	Ser	Phe	Val	Lys	Ile	Pro	Gly	Glu	Lys	Asp	Ser	Val	Ile	Cys
65					70					75					80
Leu	Lys	Gly	Ser	Gln	Trp	Ser	Asp	Ile	Glu	Glu	Phe	Cys	Asn	Arg	Ser
				85					90					95	
Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys	Gln	Pro	Tyr
			100						105					110	
Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu	Tyr	Glu	Cys
	115						120					125			
Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys	Leu	Thr	Cys
	130					135					140				
Leu	Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys	Lys	Lys	Lys
145					150					155					160
Ser	Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile	Asp	Val	Pro
			165						170				175		
Gly	Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys	Asn	Thr	Gly
		180						185					190		
Tyr	Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile	Ser	Gly	Ser
	195					200						205			
Ser	Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu	Ile	Tyr	Cys
	210					215					220				
Pro	Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly	Glu	Arg	Asp
225					230					235					240
His	Tyr	Gly	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn	Lys	Gly	Phe
			245						250					255	
Thr	Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	Asn	Asn	Asp	Glu
	260						265						270		
Gly	Glu	Trp	Ser	Gly	Pro	Pro	Pro	Glu	Cys	Arg	Gly	Lys	Ser	Leu	Thr
	275						280					285			
Ser	Lys	Val	Pro	Pro	Thr	Val	Gln	Lys	Pro	Thr	Thr	Val	Asn	Val	Pro
	290					295					300				
Thr	Thr	Glu	Val	Ser	Pro	Thr	Ser	Gln	Lys	Thr	Thr	Thr	Lys	Thr	Thr
305					310					315					320
Thr	Pro	Asn	Ala	Gln	Ala	Thr	Arg	Ser	Thr	Pro	Val	Ser	Arg	Thr	Thr
			325						330					335	
Lys	His	Phe	His	Glu	Thr	Thr	Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser
		340						345					350		
Gly	Thr	Thr	Arg	Leu	Leu	Ser	Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly
	355						360						365		
Leu	Leu	Gly	Thr	Leu	Val	Thr	Met	Gly	Leu	Leu	Thr				
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<210> 3
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3
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gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaag 120
tttgagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaatga gctaacgtac 180
tactgctgca agaaggacct gtgtaacttt aacgaacagc ttgaaaatgg tgggacatcc 240
ttatcagaga aaacagttct tctgctggtg actccatttc tggcagcagc ctggagcctt 300
catccc 306

<210> 4
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
1 5 10 15
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro
20 25 30
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala
35 40 45
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys
50 55 60
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn
65 70 75 80
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu
85 90 95
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu
100 105 110
Leu Val Thr Pro Phe Leu Ala Ala Trp Ser Leu His Pro
115 120 125

<210> 5
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5
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attgctggtt gtagcgtgat aaggtagcgt tggtcaggta ccttccgcct cattggagaa 120

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aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtagc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tgggtgtcaag caaataatat gtggggggccg 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatggt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctgggtta cttgcttggt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc cccacatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
caggaggttg cttggaccaaa aatgccagta tgtggaggtg ggtcgggtgg cggcggtacc 780
gactgtggcc tccccccaga tgtacctaat gccagccag ctttgaagg ccgtacaagt 840
tttcccagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 900
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc 960
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 1020
actcagaatt attttccagt cgggtactgt gtggaatatg agtgccgtcc aggttacaga 1080
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 1140
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaag tggtcagatt 1200
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 1260
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 1320
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 1380
ataattcaag gggaaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 1440
aaaggattca ccatgattgg agagcactct atttattgta ctgtg 1485

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<210> 6

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 6

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Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
 1             5             10             15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
      20             25             30
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
      35             40             45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
      50             55             60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
      65             70             75             80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
      85             90             95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
      100            105            110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
      115            120            125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
      130            135            140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
      145            150            155            160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
      165            170            175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu

```



```

acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgata 420
cacaatggac atcacacaag tgagaatggt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctgggta cttgcttggt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc cccacatgt gaagaggcac gctgtaaata tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaaacttt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
caggaggttg cttggaccaa aatgccagta tggtcaggag gaggaggttc cctgcagtgc 780
tacaactgtc ctaacccaac tgctgactgc aaaacagccg tcaattgttc atctgatttt 840
gatgcgtgtc tcattaccaa agctgggtta caagtgtata acaagtgttg gaagtttgag 900
cattgcaatt tcaacgacgt cacaaccgcg ttgagggaaa atgagctaac gtactactgc 960
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<210> 8

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

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Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
20          25          30
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
35          40          45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
50          55          60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
65          70          75          80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
85          90          95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
100          105          110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
115          120          125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
130          135          140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
145          150          155          160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
165          170          175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
180          185          190
Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
195          200          205
Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
210          215          220
Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
225          230          235          240
Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Ser Gly Gly Gly Gly
245          250          255
Ser Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr
260          265          270
Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala

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275		280		285											
Gly	Leu	Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe
290		295		300											
Asn	Asp	Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys
305		310		315		320									
Cys	Lys	Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn		
		325		330											

<210> 9

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

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gagaaggact cagtgatctg ccttaagggc agtcaatggc cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt atttccagtc cgggtactgtt gtggaatatg agtgccgtcc aggttacaga 3

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